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1	55	((two adj hybrid) near4 (bacteria or bacterial))	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 16:18
2	2513	enzyme near3 domain	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 16:18
3	0	((two adj hybrid) near4 (bacteria or bacterial)) near8 (enzyme near3 domain)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 16:19
4	12	((two adj hybrid) near4 (bacteria or bacterial)) and (enzyme near3 domain)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2004/02/04 16:19

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56 FILES SEARCHED...
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87 FILES SEARCHED...

L1 520 (TWO HYBRID) (4A) (BACTERIA OR BACTERIAL)

=> s l1 (10A) (enzyme (3A) domain)

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47 FILES SEARCHED...
79 FILES SEARCHED...

L2 1 L1 (10A) (ENZYME (3A) DOMAIN)

=> s l1 and (enzyme (3A) domain)

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L4 ANSWER 1 OF 17 USPATFULL on STN

AN 2004:7768 USPATFULL

TI Targeted therapeutic proteins

IN LeBowitz, Jonathan H., Frontenac, MO, UNITED STATES

Beverley, Stephen M., Clayton, MO, UNITED STATES

PA Symbiontics, Inc. (U.S. corporation)

PI US 2004006008 A1 20040108

AI US 2002-272483 A1 20021016 (10)

RLI Continuation-in-part of Ser. No. US 2002-136841, filed on 30 Apr 2002,
PENDING

PRAI US 2001-287531P 20010430 (60)

US 2001-304609P 20010710 (60)

US 2001-329461P 20011015 (60)

US 2002-351276P 20020123 (60)

US 2002-351276P 20020123 (60)

US 2002-384452P 20020529 (60)
US 2002-386019P 20020605 (60)
US 2002-408816P 20020906 (60)
DT Utility
FS APPLICATION
LN.CNT 3120
INCL INCLM: 514/008.000
INCLS: 530/397.000; 435/069.400; 435/320.100; 435/325.000; 536/023.500;
435/317.100
NCL NCLM: 514/008.000
NCLS: 530/397.000; 435/069.400; 435/320.100; 435/325.000; 536/023.500;
435/317.100
IC [7]
ICM: C07K014-65
ICS: C07H021-04; C12P021-02; C12N005-06; A61K038-30

L4 ANSWER 2 OF 17 USPATFULL on STN
AN 2004:7076 USPATFULL
TI Targeted therapeutic proteins
IN LeBowitz, Jonathan H., Frontenac, MO, UNITED STATES
Beverley, Stephen M., Clayton, MO, UNITED STATES
Sly, William S., St. Louis, MO, UNITED STATES
PA Symbiontics, Inc. (U.S. corporation)
PI US 2004005309 A1 20040108
AI US 2002-272531 A1 20021016 (10)
PRAI US 2002-408816P 20020906 (60)
US 2002-386019P 20020605 (60)
US 2002-384452P 20020529 (60)
DT Utility
FS APPLICATION
LN.CNT 3073
INCL INCLM: 424/094.610
INCLS: 435/069.100; 435/320.100; 435/201.000; 530/350.000; 536/023.500;
435/325.000
NCL NCLM: 424/094.610
NCLS: 435/069.100; 435/320.100; 435/201.000; 530/350.000; 536/023.500;
435/325.000
IC [7]
ICM: A61K038-47
ICS: C07H021-04; C12N009-26; C07K014-705; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 3 OF 17 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 1
AN 10273076 IFIPAT;IFIUDB;IFICDB
TI COLLECTION OF PROKARYOTIC DNA FOR TWO HYBRID SYSTEMS HELICOBACTER PYLORI
PROTEIN-PROTEIN INTERACTIONS AND APPLICATION THEREOF; GENERATION OF
PREFERENTIAL NUCLEOTIDE SEQUENCE CLONES; OBTAIN NUCLEOTIDE SEQUENCES,
FRAGMENT, INSERT INTO PLASMID, TRANSFORM CELLS, RECOVER TRANSFORMED CELLS
IN Legrain Pierre (FR); Rain Jean-Christophe (FR); Selig Luc (FR)
PA Unassigned Or Assigned To Individual (68000)
PI US 2003017478 A1 20030123
AI US 2001-12819 20011030
RLI WO 2000-IB603 20000414 CONTINUATION UNKNOWN
PRAI EP 1999-401066 19990430
FI US 2003017478 20030123
DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
CLMN 87
GI 8 Figure(s).
FIG. 1 is a restriction map of the plasmid pAS2 Delta Delta which may be
used for the yeast two-hybrid system.
FIG. 2 is a restriction map of the plasmid pACTIIst which may be used for
the yeast two-hybrid system.

FIG. 3 is a restriction map of the plasmid pUT18 which may be used for the **bacterial two-hybrid** system. In this figure, each multicloning site (MCS) is detailed.

FIG. 4 is a restriction map of the plasmid pUT18C which may be used for the **bacterial two-hybrid** system. In this figure, each multicloning site (MCS) is detailed.

FIG. 5 is a restriction map of the plasmid pT25 which may be used for the **bacterial two-hybrid** system. In this figure, each multicloning site (MCS) is detailed.

FIG. 6 is a restriction map of the plasmid pKT25 which may be used for the **bacterial two-hybrid** system. In this figure, each multicloning site (MCS) is detailed.

FIG. 7 is a schematic representation of the SID registered identification method. In this figure, the less-than less-than Full-length prey protein greater-than greater-than is the Open Reading Frame where the identified prey polypeptides are included, the Selected Interaction Domain SID registered is determined by comparison of every prey polypeptide fragment.

FIG. 8 is a restriction map of the plasmid pP6 which may be used for the yeast two-hybrid system.

L4 ANSWER 4 OF 17 USPATFULL on STN
AN 2003:330210 USPATFULL
TI Protein-protein interactions in adipocyte cells (3)
IN Legrain, Pierre, Paris, FRANCE
Whiteside, Simon, Cambridge, UNITED KINGDOM
Mao, Jen-I, Palo Alto, CA, UNITED STATES
Khrebtukova, Irina, San Francisco, CA, UNITED STATES
Luo, Shujun, Berkeley, CA, UNITED STATES
PA Hybrigenics, Paris, FRANCE (non-U.S. corporation)
PI US 2003232421 A1 20031218
AI US 2002-139794 A1 20020506 (10)
PRAI US 2001-288885P 20010504 (60)
DT Utility
FS APPLICATION
LN.CNT 13515
INCL INCLM: 435/226.000
INCLS: 435/069.100; 435/007.100; 435/320.100; 435/325.000; 536/023.200;
514/001.000
NCL NCLM: 435/226.000
NCLS: 435/069.100; 435/007.100; 435/320.100; 435/325.000; 536/023.200;
514/001.000
IC [7]
ICM: A61K031-00
ICS: G01N033-53; C07H021-04; C12N009-64; C12P021-02; C12N005-06
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 5 OF 17 USPATFULL on STN
AN 2003:213743 USPATFULL
TI More protein-protein interactions in the inner ear
IN Daviet, Laurent, Paris, FRANCE
Legrain, Pierre, Paris, FRANCE
Petit, Christine, Le Plessis Robinson, FRANCE
Boeda, Batiste, Paris, FRANCE
El-Amraoui, Aziz, Paris, FRANCE
PA Hybrigenics, Paris, FRANCE (non-U.S. corporation)
PI US 2003148381 A1 20030807
AI US 2002-177191 A1 20020621 (10)
PRAI EP 2002-290277 20020205
US 2001-299848P 20010621 (60)
DT Utility
FS APPLICATION
LN.CNT 2681
INCL INCLM: 435/007.100

INCLS: 435/325.000; 435/320.100; 530/350.000; 514/001.000; 536/023.100
NCL NCLM: 435/007.100
NCLS: 435/325.000; 435/320.100; 530/350.000; 514/001.000; 536/023.100
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ICM: A61K031-00
ICS: G01N033-53; C12P021-02; C12N005-06; C07K014-47; C07H021-04
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 6 OF 17 USPATFULL on STN
AN 2003:119691 USPATFULL
TI Subcellular targeting of therapeutic proteins
IN LeBowitz, Jonathan H., Frontenac, MO, UNITED STATES
Beverley, Stephen M., Clayton, MO, UNITED STATES
PA Symbiontics, Inc. (U.S. corporation)
PI US 2003082176 A1 20030501
AI US 2002-136841 A1 20020430 (10)
PRAI US 2001-287531P 20010430 (60)
US 2001-304609P 20010710 (60)
US 2001-329461P 20011015 (60)
US 2002-351276P 20020123 (60)

DT Utility
FS APPLICATION

LN.CNT 1959

INCL INCLM: 424/143.100
INCLS: 530/388.220
NCL NCLM: 424/143.100
NCLS: 530/388.220

IC [7]
ICM: A61K039-395
ICS: C07K016-28

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 7 OF 17 USPATFULL on STN
AN 2003:79292 USPATFULL
TI Protein-protein interactions between Shigella flexneri polypeptides and
mammalian polypeptides
IN Legrain, Pierre, Paris, FRANCE
PI US 2003055220 A1 20030320
AI US 2002-43487 A1 20020111 (10)
PRAI US 2001-261130P 20010112 (60)

DT Utility
FS APPLICATION

LN.CNT 11901

INCL INCLM: 530/350.000
NCL NCLM: 530/350.000

IC [7]
ICM: C07K001-00
ICS: C07K014-00; C07K017-00

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 8 OF 17 USPATFULL on STN
AN 2003:57525 USPATFULL
TI Protein-protein interactions in adipocyte cells
IN Legrain, Pierre, Paris, FRANCE
Marullo, Stefano, Paris, FRANCE
Ralf, Jockers, Bures Sur Yvette, FRANCE
PI US 2003040089 A1 20030227
AI US 2002-38010 A1 20020102 (10)
PRAI US 2001-259377P 20010102 (60)

DT Utility
FS APPLICATION

LN.CNT 7738

INCL INCLM: 435/183.000
INCLS: 435/069.100; 435/007.100; 435/325.000; 435/320.100; 536/023.200;

702/019.000
NCL NCLM: 435/183.000
NCLS: 435/069.100; 435/007.100; 435/325.000; 435/320.100; 536/023.200;
702/019.000

IC [7]
ICM: G01N033-53
ICS: G06F019-00; G01N033-48; G01N033-50; C07H021-04; C12N009-00

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 9 OF 17 USPATFULL on STN
AN 2003:10262 USPATFULL
TI Proteins that interact with betaTrCP
IN Legrain, Pierre, Paris, FRANCE
Benarous, Richard, Paris, FRANCE
Blot, Guillaume, Sarcelles, FRANCE
Lassot, Irina, Sarcelles, FRANCE
PI US 2003007956 A1 20030109
AI US 2001-23530 A1 20011218 (10)
PRAI US 2000-256276P 20001218 (60)
DT Utility
FS APPLICATION
LN.CNT 2028

INCL INCLM: 424/093.210
INCLS: 435/183.000; 435/320.100; 435/325.000; 435/455.000; 435/069.100
NCL NCLM: 424/093.210
NCLS: 435/183.000; 435/320.100; 435/325.000; 435/455.000; 435/069.100

IC [7]
ICM: A61K048-00
ICS: C12P021-02; C12N005-06; C12N009-00

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 10 OF 17 DISSABS COPYRIGHT (C) 2004 ProQuest Information and
Learning Company; All Rights Reserved on STN
AN 2003:4246 DISSABS Order Number: AAI3051391
TI Mutants of Vitreoscilla hemoglobin: Comparison of site-directed mutants
with wild type VHb regarding functional characteristics and DNT
degradation
AU Lee, Sang, Yeol [Ph.D.]; Webster, Dale A. [adviser]; Stark, Benjamin C.
[adviser]
CS Illinois Institute of Technology (0091)
SO Dissertation Abstracts International, (2002) Vol. 63, No. 4B, p. 1683.
Order No.: AAI3051391. 82 pages.
ISBN: 0-493-65803-3.
DT Dissertation
FS DAI
LA English

L4 ANSWER 11 OF 17 BIOTECHABS COPYRIGHT 2004 THOMSON DERWENT/ISI on STN
AN 2002-12227 BIOTECHABS
TI New selected interacting domain polypeptides and polynucleotides, useful
for treating or preventing infections or pathologies caused by hepatitis
C virus (HCV) or those linked to HCV infection;
double plasmid-mediated enzyme and green fluorescent and yellow
fluorescent protein reporter gene transfer and expression in mammal
cell for infection disease therapy and gene therapy
AU LEGRAIN P; WHITESIDE S; WOJCIK J
PA HYBRIGENICS SA
PI EP 1178116 6 Feb 2002
AI EP 2000-402225 3 Aug 2000
PRAI EP 2000-402225 3 Aug 2000
DT Patent
LA English
OS WPI: 2002-208115 [27]

L4 ANSWER 12 OF 17 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 3
 AN 10207777 IFIPAT;IFIUDB;IFICDB
 TI SID NUCLEIC ACIDS AND POLYPEPTIDES SELECTED FROM A PATHOGENIC STRAIN OF
 HEPATITIS C VIRUS AND APPLICATIONS THEREOF
 IN Legrain Pierre (FR); Whiteside Simon (GB); Wojcik Jerome (FR)
 PA Unassigned Or Assigned To Individual (68000)
 PI US 2002151484 A1 20021017
 AI US 2001-921397 20010802
 PRAI EP 2000-40225 20000803
 FI US 2002151484 20021017
 DT Utility; Patent Application - First Publication
 FS CHEMICAL
 APPLICATION
 CLMN 73
 GI 14 Figure(s).

FIG. 1 consists of a general overview of HCV genome and its encoded polyprotein. The RNA coding strand is represented with a line for untranslated regions (NCR) and boxes for coding regions. Positions and enzymes responsible for cleavage are indicated above. p7 is a secondary cleavage product of E2 (adapted from HOUGHTON, 1996).
 FIG. 2 is a restriction map of the plasmid pAS2 Delta Delta which may be used for producing a recombinant "Selected Interacting Domain (SID registered)" polypeptide or a recombinant marker compound of the invention.
 FIG. 3 is a restriction map of the plasmid pACTII which may be used for producing a recombinant "Selected Interacting Domain (SID registered)".
 FIG. 4 is a restriction map of the plasmid pUT18 which may be used for producing a recombinant "Selected Interacting Domain (SID registered)".
 FIG. 5 is a restriction map of the plasmid pUT18C which may be used for producing a recombinant "Selected Interacting Domain (SID registered)".
 FIG. 6 is a restriction map of the plasmid pT25 which may be used for producing a recombinant "Selected Interacting Domain (SID registered)".
 FIG. 7 is a restriction map of the plasmid pKT25 which may be used for producing a recombinant "Selected Interacting Domain (SID registered)".
 FIG. 8 is an illustration of the first step of selecting a SID registered nucleic acid of the invention, wherein it is performed a selection of different sets of overlapping nucleic acids primarily selected through a two-hybrid method, in order to define pre-SID nucleic acids. Three fragments frg1, frg2 and frg3 of lengths l1, l2 and l3 respectively. Fragment l1 and l2 are clustered together if the length of intersection, I, is greater than 30% of l1 and l2. Fragment frg3 is grouped with fragments frg1 and frg2 if the length of intersection between frg1 and frg3, l', is greater than 30% of l1 and l3 and if the length of intersection between frg2 and frg3, l' greater-than greater-than, is greater than 30% of l2 and l3.
 FIG. 9 illustrates the selection of pre-SID registered nucleic acid from a particular set of overlapping nucleic acids previously selected through a two-hybrid method. The pre-SID registered is defined as the intersection of all the fragments (frg1-6) in a cluster.
 FIG. 10 illustrates the selection of a SID registered nucleic acid from the overlapping regions between two pre-SID nucleic acids. A SID registered is defined if the length of overlap between two pre-SID registered s, l, is greater than 30 bp. Further SID registered s are defined by non-overlapping areas if their length (l') represents more than 30% of the length of one of the fragments which contributes to the corresponding preSID registered (frg1-6).
 FIG. 11 illustrates a further step of determining SID registered nucleic acids after alignment of two overlapping SID nucleic acids identified according to FIG. 10. Fragments frg1' and frg2' contribute to both SID registered 1 and SID registered 2 (top panel). For each SID registered, the number of fragments are counted and fragments are assigned to the SID registered with the most fragments. The remaining fragments are reanalysed and a new SID registered is defined as the region of intersection of these fragments (bottom panel, SID registered 2'-fragment

3' and fragment 4'.

FIG. 12 illustrates a map of the vector pB5 which may be used in example 1.

FIG. 13 illustrates a map of the vector pP6 which may be used in example 1.

L4 ANSWER 13 OF 17 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 4
AN 10163136 IFIPAT;IFIUDB;IFICDB
TI BACTERIAL MULTI-HYBRID SYSTEM AND APPLICATIONS; KIT FOR USE AS A TOOL IN
SIGNAL GENERATION IN GENETIC ENGINEERING
IN Karimova Gouzel (FR); Ladant Daniel (FR); Ullmann Agnes (FR)
PA Institut Pasteur FR (42312)
PI US 2002106783 A1 20020808
AI US 2001-973013 20011010
RLI US 1998-203681 19981201 DIVISION GRANTED
PRAI US 1997-67308P 19971204 (Provisional)
FI US 2002106783 20020808
DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
CLMN 45
GI 13 Figure(s).

FIG. 1 depicts the principle of an E. coli multi-hybrid system based on functional complementation of the catalytic domain of Bordetella adenylate cyclase (CyaA) fragments.

The upper part schematizes the basic principle of in vivo complementation between the two fragments of the catalytic domain of B. pertussis adenylate cyclase. The two boxes represent the T25 and T18 fragments corresponding to amino acids 1 to 224 and 225 to 399 of the CyaA protein. In A, the full-length catalytic domain (residues 1 to 399), when expressed in E.coli, exhibits a basal calmodulin-independent activity that results in cyclic adenosine monophosphate (cAMP) synthesis. In B, the two fragments T25 and T18, when coexpressed as independent polypeptides, are unable to interact and no cAMP synthesis occurs. In C, the two fragments, fused to two interacting proteins, X and Y, are brought into close proximity resulting in functional complementation, followed by cAMP production.

The lower part schematizes the readout of the complementation. cAMP, synthesized in an E. coli cya strain by the complementing T25 and T18 pairs, binds to the catabolite activator protein, CAP. The cAMP/CAP complex (C) can then recognize specific promoters and switch on the transcription of the corresponding genes. These reporter genes can be either natural E.coli genes, such as lacZ or mal genes, or synthetic ones, such as antibiotic resistance genes fused to a cAMP/CAP dependent promoter.

FIG. 2 is a schematic representation of plasmids.

The open boxes represent the open reading frames of betalactamase (bla) and chloramphenicol acetyl transferase (cat) genes. The dark boxes correspond to the open reading frame of cyaA' with codon numbers indicated below. The hatched boxes correspond to the multicloning site sequences (MCS) that are fused at the indicated position of the cya open reading frame. The origin of replication of the plasmids is indicated by dotted boxes.

FIG. 3.1 and FIG. 3.2 are schematic representations of other plasmids.

The left part represents the maps of the plasmids, with the different antibiotic-selectable markers (chloramphenicol acetyl transferase (cat), aminoglycoside phosphotransferase (kan) and beta-lactamase (bla), the origin of replication and the position of the multicloning site sequences (MCS) relative to the T25 and T18 open reading frames. The right part describes the nucleotide sequence of the multicloning site sequences (MCS) fused to T25 (FIG. 3.2) or T18 (FIG. 3.1) and the corresponding reading frames.

FIG. 4 depicts the results of screening of interacting proteins with the bacterial two-hybrid system.

DHPI cells were cotransformed with a mixture of plasmids pT18, pT18-zip, and PT18-Tyr, and either pT25 (A) or pT25-zip (B), plated on LB-X-Gal agar plates containing 0.5 mM IPTG, ampicillin and chloramphenicol, and incubated for 30 hrs. at 30 degrees C. Note that the cya+ colonies are larger than the cya ones.

FIG. 5 relates to the mapping of interacting domains of the B. stearotherophilus tyrosyl-tRNA synthetase.

DNA fragments encoding the indicated polypeptide segments of the tyrosyl-tRNA synthetase (the numbers correspond to the amino acid residues) were amplified by PCR using appropriate primers and cloned into pT25 and/or pT18. The functional complementation between the indicated chimeric proteins was assayed on DHP1 cells co-transformed with the corresponding plasmids by measuring the beta-galactosidase activity.

FIG. 6 relates to the mapping of interacting domains of B. pertussis B.vgA.

DNA fragments encoding indicated polypeptide segments of BvgA (the numbers correspond to the amino acid residues) were amplified by PCR using appropriate primers and cloned into pKT25 and/or pUTT18C. The functional complementation between the indicated chimeric proteins was assayed on DHP1 cells cotransformed with the corresponding plasmids by measuring the beta-galactosidase activity.

L4 ANSWER 14 OF 17 IFIPAT COPYRIGHT 2004 IFI on STN DUPLICATE 5
AN 10101671 IFIPAT;IFIUDB;IFICDB
TI **BACTERIAL TWO-HYBRID SYSTEM FOR**
PROTEIN-PROTEIN INTERACTION SCREENING, NEW STRAINS FOR USE THEREIN, AND
THEIR APPLICATIONS; KIT FOR THE MONITORING PREFERENTIAL PROTEIN
ASSOCIATIONS AND ACTIVITIES
IN Karimova Gouzel (FR); Ladant Daniel (FR); Legrain Pierre (FR); Selig Luc
(FR); Ullmann Agnes (FR)
PA Unassigned Or Assigned To Individual (68000)
PI US 2002045237 A1 20020418
AI US 2001-818939 20010328
PRAI US 2000-192886P 20000329 (Provisional)
FI US 2002045237 20020418
DT Utility; Patent Application - First Publication
FS CHEMICAL
APPLICATION
CLMN 49
GI 4 Figure(s).

FIG. 1 shows the results of zip-zip interaction in different E. coli cya strains. beta-galactosidase activity is shown for three different strains, DHM1, BHT101, and DHP1.

FIG. 2 shows the results of interaction in different strains.

beta-galactosidase activity is shown for the strains DHM1 and BTH101.

FIG. 3 is a map of plasmid pUT18C Newsfi.

FIG. 4 is a map of plasmid pKT25 Newsfi.

L4 ANSWER 15 OF 17 USPATFULL on STN
AN 2001:235087 USPATFULL
TI Bacterial multi-hybrid system and applications thereof
IN Ladant, Daniel, Cachan, France
Karimova, Gouzel, Paris, France
Ullmann, Agnes, Paris, France
PA Institut Pasteur, France (non-U.S. corporation)
PI US 6333154 B1 20011225
AI US 1998-203681 19981201 (9)
PRAI US 1997-67308P 19971204 (60)
DT Utility
FS GRANTED
LN.CNT 1394
INCL INCLM: 435/006.000
INCLS: 435/007.320; 435/029.000; 435/488.000; 435/007.600; 530/350.000
NCL NCLM: 435/006.000

NCLS: 435/007.320; 435/007.600; 435/029.000; 435/488.000; 530/350.000
IC [7]
ICM: C12Q001-68
EXF 435/7.1; 435/7.2; 435/7.32; 435/7.6; 435/7.91; 435/29; 435/440; 435/488;
435/69.1; 435/4; 435/6; 530/350; 436/63; 436/808
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L4 ANSWER 16 OF 17 WPINDEX COPYRIGHT 2004 THOMSON DERWENT on STN
AN 2000-687535 [67] WPINDEX
DNN N2000-508291 DNC C2000-209320
TI A two-hybrid system for identifying compounds useful in the treatment of
e.g. gastric ulcers comprises producing a collection of recombinant cell
clones.
DC B04 D16 T01
IN LEGRAIN, P; RAIN, J; SELIG, L
PA (HYBR-N) HYBRIGENICS SA; (LEGR-I) LEGRAIN P; (RAIN-I) RAIN J; (SELI-I)
SELIG L
CYC 22
PI WO 2000066722 A1 20001109 (200067)* EN 265p C12N015-10
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: CA JP US
EP 1173560 A1 20020123 (200214) EN C12N015-10
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
US 2003017478 A1 20030123 (200310) C12Q001-68
JP 2002542821 W 20021217 (200312) 284p C12N015-09
ADT WO 2000066722 A1 WO 2000-IB603 20000414; EP 1173560 A1 EP 2000-920989
20000414, WO 2000-IB603 20000414; US 2003017478 A1 Cont of WO 2000-IB603
20000414, US 2001-12819 20011030; JP 2002542821 W JP 2000-615746 20000414,
WO 2000-IB603 20000414
FDT EP 1173560 A1 Based on WO 2000066722; JP 2002542821 W Based on WO
2000066722
PRAI EP 1999-401066 19990430
IC ICM C12N015-09; C12N015-10; C12Q001-68
ICS A61K035-76; A61K038-00; A61K039-106; A61K039-395; A61K039-40;
A61K045-00; A61K048-00; C07K014-195; C07K014-205; C07K014-245;
C07K014-315; C07K016-12; C07K019-00; C12N001-15; C12N001-18;
C12N001-19; C12N001-21; C12N005-10; C12N015-31; C12N015-86;
C12P021-02; C12P021-08; G01N033-15; G01N033-50; G01N033-53;
G01N033-566; G06F017-00

L4 ANSWER 17 OF 17 GENBANK.RTM. COPYRIGHT 2004 on STN

LOCUS (LOC): BX321860 GenBank (R)
GenBank ACC. NO. (GBN): BX321860 AL954747
GenBank VERSION (VER): BX321860.1 GI:30180445
CAS REGISTRY NO. (RN): 509062-28-6
SEQUENCE LENGTH (SQL): 303050
MOLECULE TYPE (CI): DNA; linear
DIVISION CODE (CI): Bacteria
DATE (DATE): 23 Apr 2003
DEFINITION (DEF): Nitrosomonas europaea ATCC 19718, complete genome;
segment 5/10.
KEYWORDS (ST): complete genome
SOURCE: Nitrosomonas europaea ATCC 19718
ORGANISM (ORGN): Nitrosomonas europaea ATCC 19718
Bacteria; Proteobacteria; Betaproteobacteria;
Nitrosomonadales; Nitrosomonadaceae; Nitrosomonas
NUCLEIC ACID COUNT (NA): 75874 a 81366 c 73494 g 72316 t
REFERENCE: 1
AUTHOR (AU): Chain, P.; Lamerdin, J.; Larimer, F.; Regala, W.; Land, M.;
Hauser, L.; Hooper, A.; Klotz, M.; Norton, J.;
Sayavedra-Soto, L.; Arciero, D.; Hommes, N.; Whittaker, M.;
Arp, D.
TITLE (TI): Complete Genome Sequence of the Ammonia-Oxidizing

Bacterium and Obligate Chemolithoautotroph Nitrosomonas europaea

JOURNAL (SO): J. Bacteriol., 185 (9), 2759-2773 (2003)
OTHER SOURCE (OS): CA 138:298615
REFERENCE: 2 (bases 1 to 303050)
AUTHOR (AU): Larimer, F.
TITLE (TI): Direct Submission
JOURNAL (SO): Submitted (12-NOV-2002) Submitted on behalf of the Nitrosomonas genome consortium, the DOE Joint Genome Institute, Production Genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA, and the Genome Analysis Group, Oak Ridge National Laboratory, 1060 Commerce Park Drive, Oak Ridge, TN 37831, USA; larimerfw@ornl.gov

FEATURES (FEAT):